

Introducción a la filogenómica microbiana – GET_PHYLOMARKERS

**Microbial genome evolution –
Phylogenomics & GET_PHYLOMARKERS**

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**Introducción a la Filoinformática:
Pan-genómica y Filogenómica microbiana –
NBB & CCG-UNAM, 1-5 Agosto 2022**
<https://github.com/vinuesa/TIB-filoinfo>





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TIB2022, 1-5 Agosto, 2022 CCG-UNAM, Cuernavaca, Mor. México
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Frontiers In Microbiology Research Topics
https://github.com/vinuesa/get_phylomarkers



ORIGINAL RESEARCH article
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GET_PHYLOMARKERS, a Software Package to Select Optimal Orthologous Clusters for Phylogenomics and Inferring Pan-Genome Phylogenies, Used for a Critical Geno-Taxonomic Revision of the Genus *Stenotrophomonas*

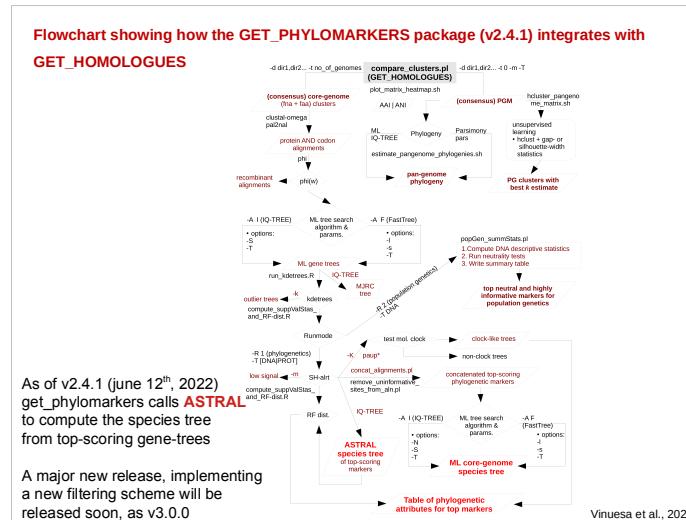
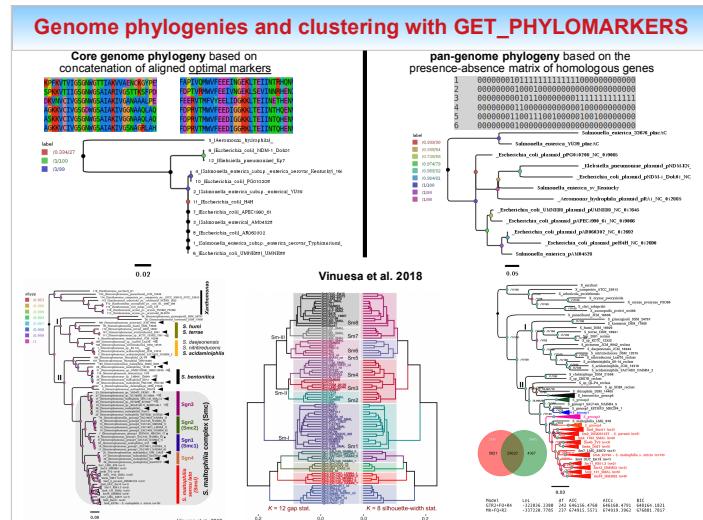

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A pipeline to select optimal markers for microbial phylogenomics and species tree estimation using coalescent and concatenation approaches
Pablo Vinuesa¹, Luz E. Ochoa-Sánchez² and Bruno Contreras-Moreira^{3,4}

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The massive accumulation of genome-sequences in public databases promoted the proliferation of genome-level phylogenetic analyses in many areas of biological research. However, due to diverse evolutionary and genetic processes, many loci have undesirable properties for phylogenetic reconstruction. These, if undetected, can result in erroneous or biased estimates, particularly when estimating species trees from concatenated datasets. To deal with these problems, we developed GET_PHYLOMARKERS, a pipeline designed to identify high-quality markers to estimate robust genome phylogenies from the orthologous clusters, or the pan-genome matrix (PGM), computed by GET_HOMOLOGUES.



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